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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/932,367A

DATE: 02/13/2002

TIME: 18:44:29

Input Set : A:\053844-5003.txt

Output Set: N:\CRF3\02132002\I932367A.raw

**ENTERED**  
*see page 5*

3 <110> APPLICANT: RHODES, Simon J.  
 4 BRIDWELL, Jeanne L.  
 5 MEIER, Bradley C.  
 6 PARKER, Gretchen E.  
 7 PRICE, Jeffrey R.  
 8 SHOWALTER, Aaron D.  
 9 SLOOP, Kyle W.  
 11 <120> TITLE OF INVENTION: GENERATION OF DIAGNOSTIC TOOLS TO ASSAY THE HUMAN  
 12 LHX3/P-LIM/LIM-3 FACTOR  
 14 <130> FILE REFERENCE: 053844-5003  
 16 <140> CURRENT APPLICATION NUMBER: 09/932,367A  
 17 <141> CURRENT FILING DATE: 2001-08-17  
 19 <150> PRIOR APPLICATION NUMBER: PCT/US00/04424  
 20 <151> PRIOR FILING DATE: 2000-02-22  
 22 <150> PRIOR APPLICATION NUMBER: US 60/121,110  
 23 <151> PRIOR FILING DATE: 1999-02-22  
 25 <160> NUMBER OF SEQ ID NOS: 113  
 27 <170> SOFTWARE: PatentIn Ver. 2.1  
 29 <210> SEQ ID NO: 1  
 30 <211> LENGTH: 1605  
 31 <212> TYPE: DNA  
 32 <213> ORGANISM: Sus scrofa  
 34 <400> SEQUENCE: 1  
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 37 cctcaagtgc agtgactgcc acacggcgct ggccgagcgc tgcttcagcc gcggagagag 180  
 38 cctctactgc aaggacgact tcttcaagcg cttcgggacc aagtgcgcgg cgtgccagct 240  
 39 gggcatcccg cccacgcagg tggtgccgc cggccaggac ttctgttacc acctgcactg 300  
 40 cttcgccctgc gtcgtgtca agcggcagct ggccacgggc gacgagttct acctcatgg 360  
 41 ggacagccgg ctcgtgtca aggccgacta cgagaccgcc aagcagcggag aggccgaggc 420  
 42 cacggccaag cggccgcgcga cgaccatcac ggccaaggcgt ctggagacgc tgaagagcgc 480  
 43 ctacaacacg tcgcccacgc cccgcgcgcga cgtgcgcgg cagtcctctcc cccgagaccgg 540  
 44 cctggacatg cgcgtcgtgc aggtgtgggt ccagaaccgc cggggccaagg aaaagcggct 600  
 45 caagaaggac gccggccggc agcgctgggg ccagtacttt cgtaacataga agcgcgcggc 660  
 46 cggggctcc aagtccggaca aggacagcgt ccaggaggag gggcaggaca gtgacgcgg 720  
 47 ggtctcccttc acagacgacg catccatggc cggaaatgggc cctgccaacg gcctctacgg 780  
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 49 gctggagcac ggaggcctgg cggggccggc gcaatggc gagctgcgcgc ccagcagcc 900  
 50 ctacgggttc ccctcgccgc cccggccctc gcagagcctc cctggccccc agccctctc 960  
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 52 gccccccaccc atgagggtgc tggcaggggaa cggaccgc tccgacatcat ccacggggag 1080  
 53 cagtgggggc taccccgact tccctgccag tcccgccctc tggctggacg aggtggatca 1140  
 54 cgctcagttc tgactgaggc cccagctccg tggagcacca gacacgagca ctgcccctgg 1200

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55 ctgggtggtc gggagccgcg ctctccttgc ccgaagccct gggcctctaa aggacacagg 1260  
 56 gtcaccggcg gggcacaggc tgaggactgt ccagcccgcc ggccctggcc ccgggcagag 1320  
 57 ggactttctc ccgggtctcga gggtccttctt gggacaaggg gagccacctg gtggctgctc 1380  
 58 agcaaggctt gtttgtaaag cagattcctc cctttatcaa caaaaattaa ctgagtgttt 1440  
 59 gctgctctt cttagaccgga gtggtcagcc cccgaagccg gggagggggg ctctccccag 1500  
 60 cccagagcag cacagccctc agactggaag atgcttaat ttttaaaatt aaaaaataat 1560  
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 65 <211> LENGTH: 383  
 66 <212> TYPE: PRT  
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 71 1 5 10 15  
 73 Ala Gly Cys Asp Gln His Ile Leu Asp Arg Phe Ile Leu Lys Ala Leu  
 74 20 25 30  
 76 Asp Arg His Trp His Ser Lys Cys Leu Lys Cys Ser Asp Cys His Thr  
 77 35 40 45  
 79 Pro Leu Ala Glu Arg Cys Phe Ser Arg Gly Glu Ser Leu Tyr Cys Lys  
 80 50 55 60  
 82 Asp Asp Phe Phe Lys Arg Phe Gly Thr Lys Cys Ala Ala Cys Gln Leu  
 83 65 70 75 80  
 85 Gly Ile Pro Pro Thr Gln Val Val Arg Arg Ala Gln Asp Phe Val Tyr  
 86 85 90 95  
 88 His Leu His Cys Phe Ala Cys Val Val Cys Lys Arg Gln Leu Ala Thr  
 89 100 105 110  
 91 Gly Asp Glu Phe Tyr Leu Met Glu Asp Ser Arg Leu Val Cys Lys Ala  
 92 115 120 125  
 94 Asp Tyr Glu Thr Ala Lys Gln Arg Glu Ala Glu Ala Thr Ala Lys Arg  
 95 130 135 140  
 97 Pro Arg Thr Thr Ile Thr Ala Lys Gln Leu Glu Thr Leu Lys Ser Ala  
 98 145 150 155 160  
 100 Tyr Asn Thr Ser Pro Lys Pro Ala Arg His Val Arg Glu Gln Leu Ser  
 101 165 170 175  
 103 Ser Glu Thr Gly Leu Asp Met Arg Val Val Gln Val Trp Phe Gln Asn  
 104 180 185 190  
 106 Arg Arg Ala Lys Glu Lys Arg Leu Lys Lys Asp Ala Gly Arg Gln Arg  
 107 195 200 205  
 109 Trp Gly Gln Tyr Phe Arg Asn Met Lys Arg Ala Arg Gly Gly Ser Lys  
 110 210 215 220  
 112 Ser Asp Lys Asp Ser Val Gln Glu Glu Gly Gln Asp Ser Asp Ala Glu  
 113 225 230 235 240  
 115 Val Ser Phe Thr Asp Glu Pro Ser Met Ala Glu Met Gly Pro Ala Asn  
 116 245 250 255  
 118 Gly Leu Tyr Gly Gly Leu Gly Glu Pro Ala Pro Ala Leu Gly Arg Pro  
 119 260 265 270  
 121 Ser Gly Ala Pro Gly Ser Phe Pro Leu Glu His Gly Gly Leu Ala Gly  
 122 275 280 285  
 124 Pro Glu Gln Tyr Gly Glu Leu Arg Pro Ser Ser Pro Tyr Gly Val Pro

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125 290 295 300  
 127 Ser Ser Pro Ala Ala Leu Gln Ser Leu Pro Gly Pro Gln Pro Leu Leu  
 128 305 310 315 320  
 130 Ser Ser Leu Val Tyr Pro Glu Ala Gly Leu Gly Leu Val Pro Ala Gly  
 131 325 330 335  
 133 Pro Pro Gly Gly Pro Pro Pro Met Arg Val Leu Ala Gly Asn Gly Pro  
 134 340 345 350  
 136 Ser Ser Asp Leu Ser Thr Gly Ser Ser Gly Gly Tyr Pro Asp Phe Pro  
 137 355 360 365  
 139 Ala Ser Pro Ala Ser Trp Leu Asp Glu Val Asp His Ala Gln Phe  
 140 370 375 380  
 143 <210> SEQ ID NO: 3  
 144 <211> LENGTH: 399  
 145 <212> TYPE: PRT  
 146 <213> ORGANISM: Mus musculus  
 148 <400> SEQUENCE: 3  
 149 Met Leu Leu Glu Ala Glu Leu Asp Cys His Arg Glu Arg Pro Gly Ala  
 150 1 5 10 15  
 152 Pro Gly Ala Ser Ala Leu Cys Thr Phe Ser Arg Thr Pro Glu Ile Pro  
 153 20 25 30  
 155 Met Cys Ala Gly Cys Asp Gln His Ile Leu Asp Arg Phe Ile Leu Lys  
 156 35 40 45  
 158 Ala Leu Asp Arg His Trp His Ser Lys Cys Leu Lys Cys Ser Asp Cys  
 159 50 55 60  
 161 His Val Pro Leu Ala Glu Arg Cys Phe Ser Arg Gly Glu Ser Val Tyr  
 162 65 70 75 80  
 164 Cys Lys Asp Asp Phe Phe Lys Arg Phe Gly Thr Lys Cys Ala Ala Cys  
 165 85 90 95  
 167 Gln Leu Gly Ile Pro Pro Thr Gln Val Val Arg Arg Ala Gln Asp Phe  
 168 100 105 110  
 170 Val Tyr His Leu His Cys Phe Ala Cys Val Val Cys Lys Arg Gln Leu  
 171 115 120 125  
 173 Ala Thr Gly Asp Glu Phe Tyr Leu Met Glu Asp Ser Arg Leu Val Cys  
 174 130 135 140  
 176 Lys Ala Asp Tyr Glu Thr Ala Lys Gln Arg Glu Ala Glu Ala Thr Ala  
 177 145 150 155 160  
 179 Lys Arg Pro Arg Thr Thr Ile Thr Ala Lys Gln Leu Glu Thr Leu Lys  
 180 165 170 175  
 182 Ser Ala Tyr Asn Thr Ser Pro Lys Pro Ala Arg His Val Arg Glu Gln  
 183 180 185 190  
 185 Leu Ser Ser Glu Thr Gly Leu Asp Arg Val Val Gln Val Trp Phe Gln  
 186 195 200 205  
 188 Asn Arg Arg Ala Lys Glu Lys Arg Leu Lys Lys Asp Ala Gly Arg Gln  
 189 210 215 220  
 191 Arg Trp Gly Gln Tyr Phe Arg Asn Met Lys Arg Ser Arg Gly Ser Ser  
 192 225 230 235 240  
 194 Lys Ser Asp Lys Asp Ser Ile Gln Glu Gly Gln Asp Ser Asp Ala Glu  
 195 245 250 255  
 197 Val Ser Phe Thr Asp Glu Pro Ser Met Ala Asp Met Gly Pro Ala Asn

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198            260            265            270  
 200 Gly Leu Tyr Ser Ser Leu Gly Glu Pro Ala Pro Ala Leu Gly Arg Pro  
 201            275            280            285  
 203 Val Gly Gly Leu Gly Ser Phe Thr Leu Asp His Gly Gly Leu Thr Gly  
 204            290            295            300  
 206 Pro Glu Gln Tyr Arg Glu Leu Arg Pro Gly Ser Pro Tyr Gly Ile Pro  
 207 305            310            315            320  
 209 Pro Ser Pro Ala Ala Pro Gln Ser Leu Pro Gly Pro Gln Pro Leu Leu  
 210            325            330            335  
 212 Ser Ser Leu Val Tyr Pro Asp Thr Asn Leu Ser Leu Val Pro Ser Gly  
 213            340            345            350  
 215 Pro Pro Gly Gly Pro Pro Pro Met Arg Val Leu Ala Gly Asn Gly Pro  
 216            355            360            365  
 218 Ser Ser Asp Leu Ser Thr Glu Ser Ser Ser Gly Tyr Pro Asp Phe Pro  
 219            370            375            380  
 221 Ala Ser Pro Ala Ser Trp Leu Asp Glu Val Asp His Ala Gln Phe  
 222 385            390            395  
 225 <210> SEQ ID NO: 4  
 226 <211> LENGTH: 395  
 227 <212> TYPE: PRT  
 228 <213> ORGANISM: Gallus gallus  
 230 <400> SEQUENCE: 4  
 231 Met Leu Leu Glu Arg Val Arg Ala Gly Ser Glu Lys Ala Ala Glu Leu  
 232    1            5            10            15  
 234 Cys Pro Phe Pro Arg Ser Pro Glu Ile Pro Leu Cys Ala Gly Cys Asn  
 235    20            25            30  
 237 Gln His Ile Val Asp Arg Phe Ile Leu Lys Val Leu Asp Arg His Trp  
 238    35            40            45  
 240 His Ser Lys Cys Leu Lys Cys Ser Asp Cys Gln Thr Gln Leu Ala Glu  
 241    50            55            60  
 243 Lys Cys Phe Ser Arg Gly Asp Gly Val Tyr Cys Lys Glu Asp Phe Phe  
 244    65            70            75            80  
 246 Lys Arg Phe Gly Thr Lys Cys Ala Ala Cys Gln Gln Gly Ile Pro Pro  
 247    85            90            95  
 249 Thr Gln Val Val Arg Arg Ala Gln Asp Phe Val Tyr His Leu His Cys  
 250    100            105            110  
 252 Phe Ala Cys Ile Val Cys Lys Arg Gln Leu Ala Thr Gly Asp Glu Phe  
 253    115            120            125  
 255 Tyr Leu Met Glu Asp Ser Arg Leu Val Cys Lys Ala Asp Tyr Glu Thr  
 256    130            135            140  
 258 Ala Lys Gln Arg Glu Ala Glu Ser Thr Ala Lys Arg Pro Arg Thr Thr  
 259 145            150            155            160  
 261 Ile Thr Ala Lys Gln Leu Glu Thr Leu Lys Asn Ala Tyr Asn Asn Ser  
 262    165            170            175  
 264 Pro Lys Pro Ala Arg His Val Arg Glu Gln Leu Ser Ser Glu Thr Gly  
 265    180            185            190  
 267 Leu Asp Met Arg Val Val Gln Val Trp Phe Gln Asn Arg Arg Ala Lys  
 268    195            200            205  
 270 Glu Lys Arg Leu Lys Lys Asp Ala Gly Arg Gln Arg Trp Gly Gln Tyr

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271 210 215 220  
 273 Phe Arg Asn Met Lys Arg Ser Arg Gly Thr Ser Lys Ser Asp Lys Asp  
 274 225 230 235 240  
 276 Ser Ile Gln Glu Glu Gly Pro Asp Ser Asp Ala Glu Val Ser Phe Thr  
 277 245 250 255  
 279 Asp Glu Pro Ser Met Ser Glu Met Ser His Ser Asn Gly Ile Tyr Ser  
 280 260 265 270  
 282 Asn Leu Ser Glu Ala Ser Pro Ala Leu Gly Arg Gln Ala Gly Thr Asn  
 283 275 280 285  
 285 Gly Gly Phe Ser Leu Asp His Ser Gly Ile Pro Ala Gln Asp Gln Tyr  
 286 290 295 300  
 288 His Asp Leu Arg Ser Asn Ser Pro Tyr Gly Ile Pro Gln Ser Pro Ala  
 289 305 310 315 320  
 291 Ser Leu Gln Ala Leu Pro Gly His Gln Pro Leu Ile Ser Ser Leu Val  
 292 325 330 335  
 294 Tyr Pro Asp Ser Gly Leu Gly Ile Met Gly Gln Gly Gly Gln Gly Val  
 295 340 345 350  
 297 Pro Gln Ser Met Arg Val Leu Ala Gly Asn Gly Pro Ser Ser Asp Leu  
 298 355 360 365  
 300 Ser Thr Gly Ser Ser Gly Gly Tyr Pro Asp Phe Pro Ala Ser Pro Ala  
 301 370 375 380  
 303 Ser Trp Leu Asp Glu Val Asp His Ala Gln Phe  
 304 385 390 395  
 307 <210> SEQ ID NO: 5  
 308 <211> LENGTH: 394  
 309 <212> TYPE: PRT  
 310 <213> ORGANISM: Xenopus laevis  
 312 <400> SEQUENCE: 5  
 313 Met Leu Leu Glu Arg Val Arg Thr Gly Thr Gln Lys Ser Ser Asp Met  
 314 1 5 10 15  
 316 Cys Gly Tyr Thr Gly Ser Pro Glu Ile Pro Gln Cys Ala Gly Cys Asn  
 317 20 25 30  
 319 Gln His Ile Val Asp Arg Phe Ile Leu Lys Val Leu Asp Arg His Trp  
 320 35 40 45  
 322 His Ser Lys Cys Leu Lys Cys Asn Asp Cys Gln Ile Gln Leu Ala Glu  
 323 50 55 60  
 325 Lys Cys Phe Ser Arg Gly Asp Ser Val Tyr Cys Lys Asp Asp Phe Phe  
 326 65 70 75 80  
 328 Lys Arg Phe Gly Thr Lys Cys Ala Ala Cys Gln Gln Gly Ile Pro Pro  
 329 85 90 95  
 331 Thr Gln Val Val Arg Arg Ala Gln Glu Phe Val Tyr His Leu His Cys  
 332 100 105 110  
 334 Phe Ala Cys Ile Val Cys Lys Arg Gln Leu Ala Thr Gly Asp Glu Phe  
 335 115 120 125  
 337 Tyr Leu Met Glu Asp Ser Arg Leu Val Cys Lys Ala Asp Tyr Glu Thr  
 338 130 135 140  
 340 Ala Lys Gln Arg Glu Ala Glu Ser Thr Ala Lys Arg Pro Arg Thr Thr  
 341 145 150 155 160  
 343 Ile Thr Ala Lys Gln Leu Glu Thr Leu Lys Asn Ala Tyr Asn Asn Ser



Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

## VERIFICATION SUMMARY

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Input Set : A:\053844-5003.txt

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L:473 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (7) SEQUENCE:  
L:477 M:283 W: Missing Blank Line separator, <400> field identifier  
L:478 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (8) SEQUENCE:  
L:980 M:283 W: Missing Blank Line separator, <400> field identifier  
L:981 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (17) SEQUENCE:  
L:985 M:283 W: Missing Blank Line separator, <400> field identifier  
L:986 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (18) SEQUENCE:  
L:1319 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:1404 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:1602 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1603 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (30) SEQUENCE:  
L:1620 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1621 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (32) SEQUENCE: